

METHOD AND APPARATUS FOR EXTRACTING AND
EVALUATING MUTUALLY SIMILAR PORTIONS IN
ONE-DIMENSIONAL SEQUENCES IN MOLECULES AND/OR
THREE-DIMENSIONAL STRUCTURES OF MOLECULES

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ABSTRACT OF THE DISCLOSURE

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15 In the analysis of one-dimensional sequences of
molecules, the longest common subsequence, the number
of elements constituting the subsequence, and
appearance positions of the subsequence are determined
by a novel and simple method, and processes, such as
homology decision, homology search, motif search and
alignment are performed based on the results. In the
analysis of these-dimensional structures of molecules,
limiting conditions, such as geometrical arrangements
of elements, are introduced to realize the
determination of correspondence of three-dimensional
structures at high speeds, and whereby it is made
possible to achieve such processing as superposed
display of three-dimensional structure of molecules,
retrieval of three-dimensional structure, and
evaluation of functions. Moreover, the molecules are
divided into secondary structure that are then related
to each other based on spatial similarity among the
secondary structures. Furthermore, similarity among
the molecules is decided based on a relationship of
spatial positions of the corresponding secondary
structures.

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